



#5

# SEQUENCE LISTING

<110> Macrozyme  
Aerts, Johannes M.F.G.  
Boot, Rolf G.

<120> A mammalian mucinase, its recombinant production, and its use in therapy or prophylaxis against diseases in which mucus is involved or infection diseases

<130> 2183-5136US

<140> 10/004,219

<141> 2001-11-02

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 476

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: human AMCase amino acid sequence deduced from cDNA sequence

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Gln Leu Gly Ser Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala  
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Gln Tyr Arg Pro Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro  
35 40 45

Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn  
50 55 60

Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe  
65 70 75 80

Asn Gly Leu Lys Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile  
85 90 95

Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr  
100 105 110

Pro Glu Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg  
115 120 125

Gln Tyr Glu Phe Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser  
130 135 140

Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln  
145 150 155 160

Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro  
165 170 175

Arg Leu Met Val Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln  
 180 185 190  
 Ser Gly Tyr Glu Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His  
 195 200 205  
 Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu  
 210 215 220  
 Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr  
 225 230 235 240  
 Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro  
 245 250 255  
 Ala Glu Lys Leu Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile  
 260 265 270  
 Leu Ser Asn Pro Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala  
 275 280 285  
 Gly Pro Ala Gly Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr  
 290 295 300  
 Glu Ile Cys Thr Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala  
 305 310 315 320  
 Pro Gln Glu Val Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr  
 325 330 335  
 Asp Asn Ile Lys Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn  
 340 345 350  
 Lys Phe Gly Gly Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr  
 355 360 365  
 Gly Thr Phe Cys Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys  
 370 375 380  
 Lys Ala Leu Gly Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro  
 385 390 395 400  
 Ile Glu Pro Ile Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly  
 405 410 415  
 Ser Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val  
 420 425 430  
 Arg Ala Asn Gly Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp  
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<213> Artificial Sequence

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<223> Description of Combined DNA/RNA Molecule: human  
AMCase cDNA sequence and deduced amino acid  
sequence

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<223> Description of Artificial Sequence: human AMCase  
cDNA sequence and deduced amino acid sequence

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<221> CDS

<222> (104)..(1531)

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                                         Met Thr Lys Leu
                                         1
att ctg ctc aca ggt ctt gtc ctt ata ctg aat ttg cag ctc ggc tct 163
Ile Leu Leu Thr Gly Leu Val Leu Ile Leu Asn Leu Gln Leu Gly Ser
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gcc tac cag ctg aca tgc tac ttc acc aac tgg gcc cag tac cgg cca 211
Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala Gln Tyr Arg Pro
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ggc ctg ggg cgc ttc atg cct gac aac atc gac ccc tgc ctc tgt acc 259
Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro Cys Leu Cys Thr
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cac ctg atc tac gcc ttt gct ggg agg cag aac aac gag atc acc acc 307
His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn Glu Ile Thr Thr
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atc gaa tgg aac gat gtg act ctc tac caa gct ttc aat ggc ctg aaa 355
Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe Asn Gly Leu Lys
                70                75                80
aat aag aac agc cag ctg aaa act ctc ctg gcc att gga ggc tgg aac 403
Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn
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ttc ggg act gcc cct ttc act gcc atg gtt tct act cct gag aac cgc 451
Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr Pro Glu Asn Arg
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cag act ttc atc acc tca gtc atc aaa ttc ctg cgc cag tat gag ttt 499
gac ggg ctg gac ttt gac tgg gag tac cct ggc tct cgt ggg agc cct 547
Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro
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cct cag gac aag cat ctc ttc act gtc ctg gtg cag gaa atg cgt gaa 595
Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln Glu Met Arg Glu
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Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro Arg Leu Met Val	
165 170 175 180	
act gct gca gta gct gct ggc atc tcc aat atc cag tct ggc tat gag	691
Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln Ser Gly Tyr Glu	
185 190 195	
atc ccc caa ctg tca cag tac ctg gac tac atc cat gtc atg acc tac	739
Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His Val Met Thr Tyr	
200 205 210	
gac ctc cat ggc tcc tgg gag ggc tac act gga gag aac agc ccc ctc	787
Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu	
215 220 225	
tac aaa tac ccg act gac acc ggc agc aac gcc tac ctc aat gtg gat	835
Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp	
230 235 240	
tat gtc atg aac tac tgg aag gac aat gga gca cca gct gag aag ctc	883
Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro Ala Glu Lys Leu	
245 250 255 260	
atc gtt gga ttc cct acc tat gga cac aac ttc atc ctg agc aac ccc	931
Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile Leu Ser Asn Pro	
265 270 275	
tcc aac act gga att ggt gcc ccc acc tct ggt gct ggt cct gct ggg	979
Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala Gly Pro Ala Gly	
280 285 290	
ccc tat gcc aag gag tct ggg atc tgg gct tac tac gag atc tgt acc	1027
Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr Glu Ile Cys Thr	
295 300 305	
ttc ctg aaa aat gga gcc act cag gga tgg gat gcc cct cag gaa gtg	1075
Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala Pro Gln Glu Val	
310 315 320	
cct tat gcc tat cag ggc aat gtg tgg gtt ggc tat gac aac atc aag	1123
Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr Asp Asn Ile Lys	
325 330 335 340	
agc ttc gat att aag gct caa tgg ctt aag cac aac aaa ttt gga ggc	1171
Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn Lys Phe Gly Gly	
345 350 355	
gcc atg gtc tgg gcc att gat ctg gat gac ttc act ggc act ttc tgc	1219
Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Thr Phe Cys	
360 365 370	
aac cag ggc aag ttt ccc cta atc tcc acc ctg aag aag gcc ctc ggc	1267
Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys Lys Ala Leu Gly	
375 380 385	
ctg cag agt gca agt tgc acg gct cca gct cag ccc att gag cca ata	1315
Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro Ile Glu Pro Ile	
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Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly Ser Ser Ser Ser	

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Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val Arg Ala Asn Gly
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ctc tac ccc gtg gca aat aac aga aat gcc ttc tgg cac tgc gtg aat 1459
Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp His Cys Val Asn
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gga gtc acg tac cag cag aac tgc cag gcc ggg ctt gtc ttc gac acc 1507
Gly Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu Val Phe Asp Thr
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agc tgt gat tgc tgc aac tgg gca taaacctgac ctggtctata ttccctagag 1561
Ser Cys Asp Cys Cys Asn Trp Ala
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<212> DNA
<213> Artificial Sequence

<220>
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        sequence

<220>
<223> Description of Artificial Sequence: mouse AMCase
        cDNA sequence and deduced amino acid sequence

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<222> (1)..(1419)

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cag ctg ggg tct gcc tac aat ctg ata tgc tat ttc acc aac tgg gcc 96
Gln Leu Gly Ser Ala Tyr Asn Leu Ile Cys Tyr Phe Thr Asn Trp Ala
    20                25                30

cag tat cgg cca ggt ctg ggg agc ttc aag cct gat gac att aac ccc 144
Gln Tyr Arg Pro Gly Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro
    35                40                45

tgc ctg tgt act cac ctg atc tat gcc ttt gct ggg atg cag aac aat 192
Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn
    50                55                60

gag atc acc acc ata gaa tgg aat gat gtt act ctc tat aaa gct ttc 240
Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe
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gga ggc tgg aac ttt gga act gct cct ttc act acc atg gtt tcc act	336
Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr	
100 105 110	
tct cag aac cgc cag acc ttc att acc tca gtc atc aaa ttt ctg cgt	384
Ser Gln Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg	
115 120 125	
cag tat ggg ttt gat gga ctg gac ctg gac tgg gaa tac cca ggc tca	432
Gln Tyr Gly Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser	
130 135 140	
cgt ggg agc cct cct cag gac aag cat ctc ttc act gtc ctg gtg aag	480
Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Lys	
145 150 155 160	
gaa atg cgt gaa gct ttt gag cag gag gct att gag agc aac agg ccc	528
Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro	
165 170 175	
aga ctg atg gtt act gct gct gta gct ggt ggg att tcc aac atc cag	576
Arg Leu Met Val Thr Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln	
180 185 190	
gct ggc tat gag atc cct gaa ctt tct aag tac ctg gat ttc atc cat	624
Ala Gly Tyr Glu Ile Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His	
195 200 205	
gtc atg aca tat gac ctc cat ggc tcc tgg gag ggc tac act ggg gag	672
Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu	
210 215 220	
aat agt cct ctt tac aaa tac cct act gag act ggt agc aat gcc tac	720
Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr	
225 230 235 240	
ctc aat gtg gat tat gtc atg aac tat tgg aag aac aat gga gcc cca	768
Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro	
245 250 255	
gct gag aag ctc att gtt gga ttc cca gag tat gga cac acc ttc atc	816
Ala Glu Lys Leu Ile Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile	
260 265 270	
ctg aga aac ccc tct gat aat gga att ggt gcc cct acc tct ggt gat	864
Leu Arg Asn Pro Ser Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp	
275 280 285	
ggc cct gct ggc gcc tat acc aga cag gct ggg ttc tgg gcc tac tat	912
Gly Pro Ala Gly Ala Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr	
290 295 300	
gag att tgc acc ttt ctg aga agt gga gcc act gag gtc tgg gat gcc	960
Glu Ile Cys Thr Phe Leu Arg Ser Gly Ala Thr Glu Val Trp Asp Ala	
305 310 315 320	

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Ser Gln Glu Val Pro Tyr Ala Tyr Lys Ala Asn Glu Trp Leu Gly Tyr	
325 330 335	
gac aat atc aag agc ttc agt gtt aag gct cag tgg ctt aag cag aac	1056
Asp Asn Ile Lys Ser Phe Ser Val Lys Ala Gln Trp Leu Lys Gln Asn	
340 345 350	
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Asn Phe Gly Gly Ala Met Ile Trp Ala Ile Asp Leu Asp Asp Phe Thr	
355 360 365	
ggc tct ttc tgt gat cag gga aaa ttt cct ctg act tct act ttg aac	1152
Gly Ser Phe Cys Asp Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn	
370 375 380	
aaa gcc ctt ggc ata tcc act gaa ggt tgc aca gct cct gac gtg cct	1200
Lys Ala Leu Gly Ile Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro	
385 390 395 400	
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Ser Glu Pro Val Thr Thr Pro Pro Gly Ser Gly Ser Gly Gly Gly Ser	
405 410 415	
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Gly Leu Tyr Pro Val Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile	
435 440 445	
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Asn Gly Ile Thr Tyr Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp	
450 455 460	
acc agc tgt aat tgc tgc aac tgg cca tgaacctaat gccattcttc	1439
Thr Ser Cys Asn Cys Cys Asn Trp Pro	
465 470	
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<223> Description of Artificial Sequence: mouse AMCase  
amino acid sequence deduced from cDNA sequence

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Gln Tyr Arg Pro Gly Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro
35 40 45

Cys	Leu	Cys	Thr	His	Leu	Ile	Tyr	Ala	Phe	Ala	Gly	Met	Gln	Asn	Asn		
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Gly	Gly	Trp	Asn	Phe	Gly	Thr	Ala	Pro	Phe	Thr	Thr	Met	Val	Ser	Thr		
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Arg	Gly	Ser	Pro	Pro	Gln	Asp	Lys	His	Leu	Phe	Thr	Val	Leu	Val	Lys		
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Arg	Leu	Met	Val	Thr	Ala	Ala	Val	Ala	Gly	Gly	Ile	Ser	Asn	Ile	Gln		
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Ala	Gly	Tyr	Glu	Ile	Pro	Glu	Leu	Ser	Lys	Tyr	Leu	Asp	Phe	Ile	His		
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Val	Met	Thr	Tyr	Asp	Leu	His	Gly	Ser	Trp	Glu	Gly	Tyr	Thr	Gly	Glu		
	210					215					220						
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225					230					235					240		
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Gly	Pro	Ala	Gly	Ala	Tyr	Thr	Arg	Gln	Ala	Gly	Phe	Trp	Ala	Tyr	Tyr		
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Asp	Asn	Ile	Lys	Ser	Phe	Ser	Val	Lys	Ala	Gln	Trp	Leu	Lys	Gln	Asn		
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Asn	Phe	Gly	Gly	Ala	Met	Ile	Trp	Ala	Ile	Asp	Leu	Asp	Asp	Phe	Thr		
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Gly Ser Phe Cys Asp Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn  
 370 375 380

Lys Ala Leu Gly Ile Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro  
 385 390 395 400

Ser Glu Pro Val Thr Thr Pro Pro Gly Ser Gly Ser Gly Gly Gly Ser  
 405 410 415

Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp  
 420 425 430

Gly Leu Tyr Pro Val Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile  
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Asn Gly Ile Thr Tyr Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp  
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Thr Ser Cys Asn Cys Cys Asn Trp Pro  
 465 470

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 <223> Description of Artificial Sequence: A-tail primer

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 <222> (1)..(22)

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 primer MAS1

<220>  
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<210> 8

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<222> (1)..(452)

<223> /note="Mouse AMCase"

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Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn Glu Ile Thr Thr Ile  
35 40 45

Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe Asn Asp Leu Lys Asn  
50 55 60

Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe  
65 70 75 80

Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr Ser Gln Asn Arg Gln  
85 90 95

Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Gly Phe Asp  
100 105 110

Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro Pro

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Phe	Glu	Gln	Glu	Ala	Ile	Glu	Ser	Asn	Arg	Pro	Arg	Leu	Met	Val	Thr
145					150					155					160
Ala	Ala	Val	Ala	Gly	Gly	Ile	Ser	Asn	Ile	Gln	Ala	Gly	Tyr	Glu	Ile
				165					170					175	
Pro	Glu	Leu	Ser	Lys	Tyr	Leu	Asp	Phe	Ile	His	Val	Met	Thr	Tyr	Asp
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Leu	His	Gly	Ser	Trp	Glu	Gly	Tyr	Thr	Gly	Glu	Asn	Ser	Pro	Leu	Tyr
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Lys	Tyr	Pro	Thr	Glu	Thr	Gly	Ser	Asn	Ala	Tyr	Leu	Asn	Val	Asp	Tyr
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Val	Met	Asn	Tyr	Trp	Lys	Asn	Asn	Gly	Ala	Pro	Ala	Glu	Lys	Leu	Ile
225					230					235					240
Val	Gly	Phe	Pro	Glu	Tyr	Gly	His	Thr	Phe	Ile	Leu	Arg	Asn	Pro	Ser
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Asp	Asn	Gly	Ile	Gly	Ala	Pro	Thr	Ser	Gly	Asp	Gly	Pro	Ala	Gly	Ala
			260					265					270		
Tyr	Thr	Arg	Gln	Ala	Gly	Phe	Trp	Ala	Tyr	Tyr	Glu	Ile	Cys	Thr	Phe
		275					280					285			
Leu	Arg	Ser	Gly	Ala	Thr	Glu	Val	Trp	Asp	Ala	Ser	Gln	Glu	Val	Pro
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Phe	Ser	Val	Lys	Ala	Gln	Trp	Leu	Lys	Gln	Asn	Asn	Phe	Gly	Gly	Ala
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Met	Ile	Trp	Ala	Ile	Asp	Leu	Asp	Asp	Phe	Thr	Gly	Ser	Phe	Cys	Asp
			340					345					350		
Gln	Gly	Lys	Phe	Pro	Leu	Thr	Ser	Thr	Leu	Asn	Lys	Ala	Leu	Gly	Ile
		355					360					365			
Ser	Thr	Glu	Gly	Cys	Thr	Ala	Pro	Asp	Val	Pro	Ser	Glu	Pro	Val	Thr
		370				375					380				
Thr	Pro	Pro	Gly	Ser	Gly	Ser	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser
385					390					395					400
Gly	Gly	Ser	Gly	Phe	Cys	Ala	Asp	Lys	Ala	Asp	Gly	Leu	Tyr	Pro	Val
				405					410					415	
Ala	Asp	Asp	Arg	Asn	Ala	Phe	Trp	Gln	Cys	Ile	Asn	Gly	Ile	Thr	Tyr
			420					425					430		
Gln	Gln	His	Cys	Gln	Ala	Gly	Leu	Val	Phe	Asp	Thr	Ser	Cys	Asn	Cys
		435					440					445			

Cys Asn Trp Pro  
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Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp Pro Ser Leu Cys Thr His  
20 25 30  
Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn His Gln Leu Ser Thr Thr  
35 40 45  
Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu Phe Asn Gly Leu Lys Lys  
50 55 60  
Met Asn Pro Lys Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe  
65 70 75 80  
Gly Thr Gln Lys Phe Thr Asp Met Val Ala Thr Ala Asn Asn Arg Gln  
85 90 95  
Thr Phe Val Asn Ser Ala Ile Arg Phe Leu Arg Lys Tyr Ser Phe Asp  
100 105 110  
Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Gln Gly Ser Pro Ala  
115 120 125  
Val Asp Lys Glu Arg Phe Thr Thr Leu Val Gln Asp Leu Ala Asn Ala  
130 135 140  
Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys Glu Arg Leu Leu Leu Ser  
145 150 155 160  
Ala Ala Val Pro Ala Gly Gln Thr Tyr Val Asp Ala Gly Tyr Glu Val  
165 170 175  
Asp Lys Ile Ala Gln Asn Leu Asp Phe Val Asn Leu Met Ala Tyr Asp  
180 185 190  
Phe His Gly Ser Trp Glu Lys Val Thr Gly His Asn Ser Pro Leu Tyr  
195 200 205  
Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser Leu Asn Val Asp Ala  
210 215 220  
Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro Ala Ser Lys Leu Ile  
225 230 235 240

Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr Leu Ala Ser Ser Ser  
 245 250 255  
 Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser Gly Thr Pro Gly Pro  
 260 265 270  
 Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr Glu Val Cys Ser Trp  
 275 280 285  
 Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln Lys Val Pro Tyr Ile  
 290 295 300  
 Phe Arg Asp Asn Gln Trp Val Gly Phe Asp Asp Val Glu Ser Phe Lys  
 305 310 315 320  
 Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly Leu Gly Gly Ala Met Val  
 325 330 335  
 Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly Phe Ser Cys Asn Gln Gly  
 340 345 350  
 Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln Glu Leu Ser Leu Pro Tyr  
 355 360 365  
 Leu Pro Ser Gly Thr Pro Glu Leu Glu Val Pro Lys Pro Gly Gln Pro  
 370 375 380  
 Ser Glu Pro Glu His Gly Pro Ser Pro Gly Gln Asp Thr Phe Cys Gln  
 385 390 395 400  
 Gly Lys Ala Asp Gly Leu Tyr Pro Asn Pro Arg Glu Arg Ser Ser Phe  
 405 410 415  
 Tyr Ser Cys Ala Ala Gly Arg Leu Phe Gln Gln Ser Cys Pro Thr Gly  
 420 425 430  
 Leu Val Phe Ser Asn Ser Cys Lys Cys Cys Thr Trp Asn  
 435 440 445

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

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<220>

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<222> (1)..(24)

<400> 11

tctgacagca cagaatccac tgcc

24

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

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 <223> Description of Artificial Sequence: primer  
 HAS3-A-tail  
  
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 <210> 13  
 <211> 22  
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 1 5 10 15  
 Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro Cys Leu Cys Thr His  
 20 25 30  
 Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn Glu Ile Thr Thr Ile  
 35 40 45  
 Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe Asn Gly Leu Lys Asn  
 50 55 60  
 Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe  
 65 70 75 80  
 Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr Pro Glu Asn Arg Gln  
 85 90 95  
 Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Glu Phe Asp  
 100 105 110  
 Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro Pro

115					120					125				
Gln Asp Lys His Leu Phe Thr Val Leu Val Gln Glu Met Arg Glu Ala	130				135					140				
Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro Arg Leu Met Val Thr	145				150				155					160
Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln Ser Gly Tyr Glu Ile				165				170					175	
Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His Val Met Thr Tyr Asp			180				185					190		
Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu Tyr		195					200				205			
Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp Tyr	210					215				220				
Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro Ala Glu Lys Leu Ile	225				230				235					240
Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile Leu Ser Asn Pro Ser				245				250					255	
Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala Gly Pro Ala Gly Pro			260				265					270		
Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr Glu Ile Cys Thr Phe		275					280				285			
Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala Pro Gln Glu Val Pro	290					295				300				
Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr Asp Asn Ile Lys Ser	305				310				315					320
Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn Lys Phe Gly Gly Ala				325				330					335	
Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Thr Phe Cys Asn			340				345					350		
Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys Lys Ala Leu Gly Leu		355					360					365		
Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro Ile Glu Pro Ile Thr		370				375				380				
Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly Ser Ser Ser Ser Gly	385				390				395					400
Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val Arg Ala Asn Gly Leu				405				410					415	
Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp His Cys Val Asn Gly			420				425					430		
Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu Val Phe Asp Thr Ser		435				440					445			

Cys Asp Cys Cys Asn Trp Ala  
450 455